SEQUENCE LISTING

<110> Harvey, Diane Marie
       Yang, Yi
       Kohl, Nancy

<120> ISOLATED NUCLEIC ACID MOLECULE ENCODING
    A NOVEL CENTROMERE-ASSOCIATED MOTOR PROTEIN, AND USES
    THEREOF

<130> 21023P

<150> PCT/US03/18203
<151> 2003-06-09

<150> 60/387,403
<151> 2002-06-10

<160> 4

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Human

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<213> Human

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Thr Asp Asn Asn Val Ile Tyr Gln Val Asp Gly Ser Lys Ser Phe Asn
        35                  40                  45
Phe Asp Arg Val Phe His Gly Asn Glu Thr Thr Lys Asn Val Tyr Glu
        50                  55                  60
Glu Ile Ala Ala Pro Ile Ile Asp Ser Ala Ile Gln Gly Tyr Asn Gly
65                  70                  75                  80
Thr Ile Phe Ala Tyr Gly Gln Thr Ala Ser Gly Lys Thr Tyr Thr Met
            85                  90                  95
Met Gly Ser Glu Asp His Leu Gly Val Ile Pro Arg Ala Ile His Asp
            100                 105                 110
Ile Phe Gln Lys Ile Lys Lys Phe Pro Asp Arg Glu Phe Leu Leu Arg
        115                 120                 125
Val Ser Tyr Met Glu Ile Tyr Asn Glu Thr Ile Thr Asp Leu Leu Cys
        130                 135                 140
Gly Thr Gln Lys Met Lys Pro Leu Ile Ile Arg Glu Asp Val Asn Arg
145                 150                 155                 160
Asn Val Tyr Val Ala Asp Leu Thr Glu Glu Val Val Tyr Thr Ser Glu
            165                 170                 175
Met Ala Leu Lys Trp Ile Thr Lys Gly Glu Lys Ser Arg His Tyr Gly
            180                 185                 190
Glu Thr Lys Met Asn Gln Arg Ser Ser Arg Ser His Thr Ile Phe Arg
        195                 200                 205
Met Ile Leu Glu Ser Arg Glu Lys Gly Glu Pro Ser Asn Cys Glu Gly
        210                 215                 220
Ser Val Lys Val Ser His Leu Asn Leu Val Asp Leu Ala Gly Ser Glu
225                 230                 235                 240
Arg Ala Ala Gln Thr Gly Ala Ala Gly Val Arg Leu Lys Glu Gly Cys
            245                 250                 255
Asn Ile Asn Arg Ser Leu Phe Ile Leu Gly Gln Val Ile Lys Lys Leu
            260                 265                 270
Ser Asp Gly Gln Val Gly Gly Phe Ile Asn Tyr Arg Asp Ser Lys Leu
        275                 280                 285
Thr Arg Ile Leu Gln Asn Ser Leu Gly Gly Asn Ala Lys Thr Arg Ile
        290                 295                 300
Ile Cys Thr Ile Thr Pro Val Ser Phe Asp Glu Thr Leu Thr Ala Leu
305                 310                 315                 320
Gln Phe Ala Ser Thr Ala Lys Tyr Met Lys Asn Thr Pro Tyr Val Asn
            325                 330                 335
Glu Val Ser Thr Asp Glu Ala Leu Leu Lys Arg Tyr Arg Lys Glu Ile
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Met Asp Leu Lys Lys Gln Leu Glu Glu Val Ser Leu Glu Thr Arg Ala
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Leu Val Thr Ser Ser Ser Leu Thr Leu Gln Gln Glu Leu Lys Ala Lys
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Arg Lys Arg Arg Val Thr Trp Cys Leu Gly Lys Ile Asn Lys Met Lys
        420             425             430
Asn Ser Asn Tyr Ala Asp Gln Phe Asn Ile Pro Thr Asn Ile Thr Thr
        435             440             445
Lys Thr His Lys Leu Ser Ile Asn Leu Leu Arg Glu Ile Asp Glu Ser
    450             455             460
Val Gly Thr Ile Trp Glu Phe Glu Ala Tyr Val Glu Gln Lys Leu Ile
465             470             475             480
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gatcatttgg gagttatacc cagggcaatt catgacattt ccaaaaaat taagaagttt 360
cctgataggg aatttctctt acgtgtatct tacatggaaa tatacaatga aaccattaca 420
gatttactct gtggcactca aaaaatgaaa cctttaatta ttcgagaaga tgtcaatagg 480
aatgtgtatg ttgctgatct cacagaagaa gttgtatata catcagaaat ggctttgaaa 540
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aattgtgaag gatctgttaa ggtatcccat ttgaatttgg ttgatcttgc aggcagtgaa 720
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agcttatta ttttgggaca agtgatcaag aaacttagtg atggacaagt tggtggtttc 840
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cagtttgcca gtactgctaa atatatgaag aatactcctt atgttaatga ggtatcaact 1020
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<211> 355
<212> PRT
<213> Human

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Asn Ser Arg Glu Glu Ser Leu Gly Glu Thr Ala Gln Val Tyr Trp Lys
            20              25              30
Thr Asp Asn Asn Val Ile Tyr Gln Val Asp Gly Ser Lys Ser Phe Asn
            35              40              45
```

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Phe Asp Arg Val Phe His Gly Asn Glu Thr Thr Lys Asn Val Tyr Glu
    50                  55                  60
Glu Ile Ala Ala Pro Ile Ile Asp Ser Ala Ile Gln Gly Tyr Asn Gly
65                  70                  75                  80
Thr Ile Phe Ala Tyr Gly Gln Thr Ala Ser Gly Lys Thr Tyr Thr Met
                85                  90                  95
Met Gly Ser Glu Asp His Leu Gly Val Ile Pro Arg Ala Ile His Asp
            100                 105                 110
Ile Phe Gln Lys Ile Lys Lys Phe Pro Asp Arg Glu Phe Leu Leu Arg
        115                 120                 125
Val Ser Tyr Met Glu Ile Tyr Asn Glu Thr Ile Thr Asp Leu Leu Cys
    130                 135                 140
Gly Thr Gln Lys Met Lys Pro Leu Ile Ile Arg Glu Asp Val Asn Arg
145                 150                 155                 160
Asn Val Tyr Val Ala Asp Leu Thr Glu Glu Val Val Tyr Thr Ser Glu
            165                 170                 175
Met Ala Leu Lys Trp Ile Thr Lys Gly Glu Lys Ser Arg His Tyr Gly
        180                 185                 190
Glu Thr Lys Met Asn Gln Arg Ser Ser Arg Ser His Thr Ile Phe Arg
    195                 200                 205
Met Ile Leu Glu Ser Arg Glu Lys Gly Glu Pro Ser Asn Cys Glu Gly
    210                 215                 220
Ser Val Lys Val Ser His Leu Asn Leu Val Asp Leu Ala Gly Ser Glu
225                 230                 235                 240
Arg Ala Ala Gln Thr Gly Ala Ala Gly Val Arg Leu Lys Glu Gly Cys
            245                 250                 255
Asn Ile Asn Arg Ser Leu Phe Ile Leu Gly Gln Val Ile Lys Lys Leu
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Ser Asp Gly Gln Val Gly Gly Phe Ile Asn Tyr Arg Asp Ser Lys Leu
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Thr Arg Ile Leu Gln Asn Ser Leu Gly Gly Asn Ala Lys Thr Arg Ile
    290                 295                 300
Ile Cys Thr Ile Thr Pro Val Ser Phe Asp Glu Thr Leu Thr Ala Leu
305                 310                 315                 320
Gln Phe Ala Ser Thr Ala Lys Tyr Met Lys Asn Thr Pro Tyr Val Asn
            325                 330                 335
Glu Val Ser Thr Val Asp Lys Leu Ala Ala Ala Leu Glu His His His
            340                 345                 350
His His His
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